

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Bandman, Olga
Guegler, Karl J.
Lal, Preeti

(ii) TITLE OF THE INVENTION: SH3-CONTAINING PROTEINS

(iii) NUMBER OF SEQUENCES: 5

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
(B) STREET: 3174 Porter Dr.
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: USA
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Filed Herewith

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Billings, Lucy J.
(B) REGISTRATION NUMBER: 36,749
(C) REFERENCE/DOCKET NUMBER: PF-0419 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 265 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: BRAITUT03
(B) CLONE: 865744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Lys	Arg	Thr	Val	Ser	Asp	Asn	Ser	Leu	Ser	Asn	Ser	Arg	Gly	Glu
1				5					10					15	
Gly	Lys	Pro	Asp	Leu	Lys	Phe	Gly	Gly	Lys	Ser	Lys	Gly	Lys	Leu	Trp
			20					25					30		
Pro	Phe	Ile	Lys	Lys	Asn	Lys	Gly	Ala	Thr	Pro	Glu	Asp	Phe	Ser	Asn
			35				40					45			
Leu	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	Lys	Val	Asp	Glu

50	55	60
Leu Asn Lys Glu Ile Gln Lys Glu Met Asp Gln Arg Asp Ala Ile Thr		
65	70	75
Lys Met Lys Asp Val Tyr Leu Lys Asn Pro Gln Met Gly Asp Pro Ala		80
	85	90
Ser Leu Asp His Lys Leu Ala Glu Val Ser Gln Asn Ile Glu Lys Leu		95
	100	105
Arg Val Glu Thr Gln Lys Phe Glu Ala Trp Leu Ala Glu Val Glu Gly		110
	115	120
Arg Leu Pro Ala Arg Asn Glu Gln Ala Arg Arg Gln Ser Gly Leu Tyr		125
	130	135
Asp Ser Gln Asn Pro Pro Thr Val Asn Asn Cys Ala Gln Asp Arg Glu		140
	145	150
Ser Pro Asp Gly Ser Tyr Thr Glu Glu Gln Ser Gln Glu Ser Glu Met		155
	165	170
Lys Val Leu Ala Thr Asp Phe Asp Asp Glu Phe Asp Asp Glu Glu Pro		175
	180	185
Leu Pro Ala Ile Gly Thr Cys Lys Ala Leu Tyr Thr Phe Glu Gly Gln		190
	195	200
Asn Glu Gly Thr Ile Ser Val Val Glu Gly Glu Thr Leu Tyr Val Ile		205
	210	215
Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Ile Arg Arg Asn Glu Asp		220
	225	230
Glu Glu Gly Tyr Val Pro Thr Ser Tyr Val Glu Val Cys Leu Asp Lys		235
	245	250
Asn Ala Lys Gly Ala Lys Thr Tyr Ile		255
	260	265

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1459 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BRAITUT03
- (B) CLONE: 865744

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

AGTAAAAGCA	GCCGAATCAA	TTGATCAGAA	AAATGATTCA	CAGCTGGTAA	TAGAAGCTTA	60
TAAATCAGGG	TTTGAGCCTC	CTGGAGACAT	TGAATTTGAG	GATTACACTC	AGCCAATGAA	120
GCGCACTGTG	TCAGATAACA	GCCTTTCAAA	TTCCAGAGGA	GAAGGCAAAC	CAGACCTCAA	180
ATTTGGTGGC	AAATCCAAAG	GAAAGTTATG	GCCGTTTCATC	AAAAAAAATA	AGGGTGCAAC	240
ACCGGAGGAT	TTCAAGCAAC	TCCCACCTGA	ACAAAGAAGG	AAAAAGCTGC	AGCAGAAAAGT	300
CGATGAGTTA	AATAAAGAAA	TTCAGAAGGA	GATGGATCAA	AGAGATGCCA	TAACAAAAAT	360
GAAAGATGTC	TACCTAAAGA	ATCCTCAGAT	GGGAGACCCA	GCCAGTTTGG	ATCACAAATT	420
AGCAGAAGTC	AGCCAAAATA	TAGAGAAACT	GCGAGTAGAG	ACCCAGAAAT	TTGAGGCCTG	480
GCTGGCTGAG	GTTGAAGGCC	GGCTCCCAGC	ACGCAACGAG	CAGGCGCGCC	GGCAGAGCGG	540
ACTGTACGAC	AGCCAGAACC	CACCCACAGT	CAACAACATGC	GCCCAGGACC	GTGAGAGCCC	600
AGATGGCAGT	TACACAGAGG	AGCAGAGTCA	GGAGAGTGAG	ATGAAGGTGC	TGGCCACGGA	660
TTTTGACGAC	GAGTTTGATG	ATGAGGAGCC	CCTCCCTGCC	ATAGGGACGT	GCAAAGCTCT	720
CTACACATTT	GAAGGTCAGA	ATGAAGGAAC	GATTTCCGTA	GTGAAGGAG	AAACATTGTA	780
TGTCATAGAG	GAAGACAAAG	GCGATGGCTG	GACCCGCATT	CGGAGAAATG	AAGATGAAGA	840
GGGTTATGTC	CCCACTTCAT	ATGTCGAAGT	CTGTTTGGAC	AAAAATGCCA	AAGGTGCTAA	900
GACTTATATT	TAATACCATA	AAAAAAAAAA	ACTTAAAAAA	AATGGAGTTG	TTTCTCCCCA	960
CAACCGTGAC	TGTTACAGGC	AGTTCCCTCAA	GAGACTGGCT	GGCAAGCACC	ATAATGCACG	1020
TTCTCCTGTA	GTCTCACGTG	GACTTCAGGG	TCCGGGCACC	TGAATTGCCT	TGTCTAGTTT	1080
GGGCTGTAAT	CAAGTTTCAC	TTGCTGATGA	AATTTTATGT	GGAAAGCTGC	CAACCGCCAA	1140
CTTACAGCTA	TGTCATTCAA	AATCTGATAA	ACATTTCTTC	TTTTGGCGGT	ATCTGTAGAT	1200
TAAAAAATAA	GTTGCATTGT	AGCTTCTCAT	CTTTCTGAAT	TTAAAAGCCG	GCACGCATCA	1260
TGCAGGTGCC	AAAGACTTCC	CTACTCTTGT	TTATATCTAG	TATCCACCAT	ACACTGAGCT	1320
ACATTAGGTG	GTTACAGATT	GTAACCTAAT	AAACTGAACT	GTGTTAGTTT	GTTAAATTGG	1380
ATACTCATTC	ACTTGGGGAG	GAGTCACAAG	TGAAATACCA	TCTCTTTCTT	GACTAAAGCG	1440

GTAAATAAGG TTCTTATTG

1459

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1816529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Asp Val Tyr Glu Lys Thr Pro Gln Met Gly Asp Pro Ala Ser
 1 5 10 15
 Leu Glu Pro Gln Ile Ala Glu Thr Leu Ser Asn Ile Glu Arg Leu Lys
 20 25 30
 Leu Glu Val Gln Lys Tyr Glu Ala Trp Leu Ala Glu Ala Glu Ser Arg
 35 40 45
 Val Leu Ser Asn Arg Gly Asp Ser Leu Ser Arg His Ala Arg Pro Pro
 50 55 60
 Xaa Pro Pro Ala Ser Ala Pro Pro Asp Ser Ser Asn Ser Ala Ser
 65 70 75 80
 Gln Asp Thr Lys Glu Ser Ser Glu Glu Pro Pro Ser Glu Glu Ser Gln
 85 90 95
 Asp Thr Pro Ile Tyr Thr Glu Phe Asp Glu Asp Phe Glu Glu Glu Pro
 100 105 110
 Thr Ser Pro Ile Gly His Cys Val Ala Ile Tyr His Phe Glu Gly Ser
 115 120 125
 Ser Glu Gly Thr Ile Ser Met Ala Glu Gly Glu Asp Leu Ser Leu Met
 130 135 140
 Glu Glu Asp Lys Gly Asp Gly Trp Thr Arg Val Arg Arg Lys Glu Gly
 145 150 155 160
 Gly Glu Gly Tyr Val Pro Thr Ser Tyr Leu Arg Val Thr Leu Asn
 165 170 175

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNOT20
- (B) CLONE: 1816529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ATGAACCGTG CACCCTNCGA CAGCAGTCTG GGCACCCCCT ACGGATGGAC GGNCTGAACT 60
 CCGAGGNCCG GGTCGCAGCC GCACCAAGCG CTGGNCTTTT GGCAAGAAGA ACAAGACAGT 120
 GGTGACCGAG GATTTTAGCC ACTTGCCCCC AGAGCAGCAG CGAAAACGGC TTCAACAGCA 180
 GTTGGAAGAA CGCAGTCGTG AACTTCAGAA GGAGGTTGAC CAGAGGGAAG CCCTAAAGAA 240
 AATGAAGGAT GTCTATGAGA AGACACCTCA GATGGGGGAC CCCGCCAGCT TGGAGCCCCA 300
 GATCGCTGAA ACCCTGAGCA ACATTGAACG GCTGAAATTG GAAGTGCAGA AGTATGAGGC 360
 GTGGCTGGCA GAAGCTGAAA GTCGAGTCCT TAGCAACCGG GGAGACAGCC TGAGCCGGCA 420
 CGCCCGGCCCT CCCGANCCCC CCGCTAGCGC CCCGCCAGAC AGCAGCAGCA ACAGCGCATC 480
 ACAGGACACC AAGGAGAGCT CTGAAGAGCC TCCCTCAGAA GAGAGCCAGG ACACCCCAT 540
 TTACACGGAG TTTGATGAGG ATTTTCGAGGA GGAACCCACA TCCCCCATAG GTCACTGTGT 600
 GGCCATCTAC CACTTTGAAG GGTCCAGCGA GGGCACTATC TCTATGGCCG AGGGTGAAGA 660
 CCTCAGTCTT ATGGAAGAAG ACAAAGGGGA CGGCTGGACC CGGGTCAGGC GGAAAGAGGG 720
 AGGCGAGGGC TACGTGCCCCA CCTCCTACCT CCGAGTCACG CTCAATTGAA CCC 773

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
 (B) CLONE: 1255033

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys	Ile	His	Cys	Phe	Arg	Ser	Leu	Lys	Arg	Gly	Gly	Val	Thr	Pro	Glu	1	5	10	15
Asp	Phe	Ser	Asn	Phe	Pro	Pro	Glu	Gln	Arg	Arg	Lys	Lys	Leu	Gln	Gln	20	25	30	
Lys	Val	Asp	Asp	Leu	Asn	Arg	Glu	Ile	Gln	Lys	Glu	Thr	Asp	Gln	Arg	35	40	45	
Asp	Ala	Ile	Thr	Lys	Met	Lys	Asp	Val	Tyr	Leu	Lys	Asn	Pro	Gln	Met	50	55	60	
Gly	Asp	Pro	Ala	Ser	Leu	Asp	Gln	Lys	Leu	Thr	Glu	Val	Thr	Gln	Asn	65	70	75	
Ile	Glu	Lys	Leu	Arg	Leu	Glu	Ala	Gln	Lys	Phe	Glu	Ala	Trp	Leu	Ala	85	90	95	
Glu	Val	Glu	Gly	Arg	Leu	Pro	Ala	Arg	Ser	Glu	Gln	Ala	Arg	Arg	Gln	100	105	110	
Ser	Gly	Leu	Tyr	Asp	Gly	Gln	Thr	His	Gln	Thr	Val	Thr	Asn	Cys	Ala	115	120	125	
Gln	Asp	Arg	Glu	Ser	Pro	Asp	Gly	Ser	Tyr	Thr	Glu	Glu	Gln	Ser	Gln	130	135	140	
Glu	Ser	Glu	His	Lys	Val	Leu	Ala	Pro	Asp	Phe	Asp	Asp	Glu	Phe	Asp	145	150	155	
Asp	Glu	Glu	Pro	Leu	Pro	Ala	Ile	Gly	Thr	Cys	Lys	Ala	Leu	Tyr	Thr	165	170	175	
Phe	Glu	Gly	Gln	Asn	Glu	Gly	Thr	Ile	Ser	Val	Val	Glu	Gly	Glu	Thr	180	185	190	
Leu	Ser	Val	Ile	Glu	Glu	Asp	Lys	Gly	Asp	Gly	Trp	Thr	Arg	Ile	Arg	195	200	205	
Arg	Asn	Glu	Asp	Glu	Glu	Gly	Tyr	Phe	Pro	Thr	Ser	Tyr	Val	Glu	Val	210	215	220	
Tyr	Leu	Asp	Lys	Asn	Ala	Lys	Gly	Ala	Lys	Thr	Tyr	Ile	225	230	235				